

Attach.
paper
#10

Results of BLAST

BLASTP 2.2.1 [Apr-13-2001]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1006356104-14842-14592

Query=

(131 letters)

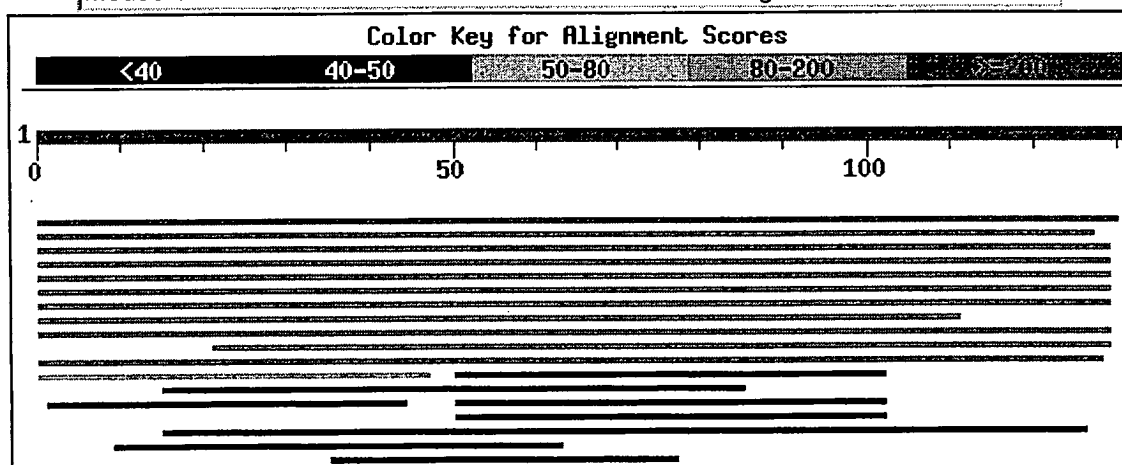
Database: nr

799,241 sequences; 254,026,857 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

Taxonomy reports**Distribution of 20 Blast Hits on the Query Sequence**

Mouse-over to show defline and scores. Click to show alignments



Sequences producing significant alignments:

Score	E
(bits)	Value

gi 7528274 gb AAF63204.1 AF244915_1	(AF244915) interleukin-...	244	1e-64
gi 14573528 gb AAK68108.1 AF385625_1	(AF385625) interleukin...	179	4e-45
gi 2905620 gb AAC03535.1	(AF043334) interleukin 13 precurs...	169	4e-42
gi 4504645 ref NP_002179.1	(NM_002188) interleukin 13 [Hom...	169	5e-42
gi 2144691 pir A47481	interleukin-13 precursor - human >gi...	167	1e-41

gi 7387804 sp Q9XSV9 IL13_BOVIN	INTERLEUKIN-13 PRECURSOR (1...	161	8e-40
gi 1127548 gb AAA83738.1	(U10307) interleukin 13 [Homo sap...	160	1e-39
gi 4558814 gb AAD22748.1 AF072807_1	(AF072807) interleukin-...	146	3e-35
gi 6680403 ref NP_032381.1	(NM_008355) interleukin 13 [Mus...	143	3e-34
gi 14719448 pdb 1GA3 A	Chain A, Nmr Structure Of Interleuki...	141	1e-33
gi 16758680 ref NP_446280.1	(NM_053828) interleukin 13 [Ra...	139	4e-33
gi 258577 gb AAB23881.1	P600 homolog [human, Peptide, 49 aa]	61	1e-09
gi 451840 gb AAA61629.1	(U05203) putative preprosperminoge...	31	1.8
gi 16760873 ref NP_456490.1	(NC_003198) flagellar transcri...	31	1.8
gi 7387658 sp O52222 FLHC_SALTY	FLAGELLAR TRANSCRIPTIONAL A...	30	2.8
gi 16765266 ref NP_460881.1	(NC_003197) regulator of flage...	30	2.9
gi 14485571 gb AAK63010.1 AF320026_1	(AF320026) heme oxygen...	30	3.6
gi 11466430 ref NP_038436.1	(NC_002186) putative plastid d...	30	4.4
gi 1293576 gb AAA98646.1	(U49765) immunoglobulin heavy cha...	30	5.4
gi 15641617 ref NP_231249.1	(NC_002505) conserved hypothet...	29	8.0

Alignments

>gi|7528274|gb|AAF63204.1|AF244915_1 (AF244915) interleukin-13 [Canis familiaris]
Length = 131

Score = 244 bits (622), Expect = 1e-64
Identities = 131/131 (100%), Positives = 131/131 (100%)

Query: 1 MALWLTVVIALTCLGGLASPSVTPSPTLKEIEELVNITQNQASLCNGSMVWSVNLTAG 60
MALWLTVVIALTCLGGLASPSVTPSPTLKEIEELVNITQNQASLCNGSMVWSVNLTAG
Sbjct: 1 MALWLTVVIALTCLGGLASPSVTPSPTLKEIEELVNITQNQASLCNGSMVWSVNLTAG 60

Query: 61 MYCAALESLINVSDCSAIQRTQRMKALCSQKPAAGQISSERSRDTKIEVIQLVKNLLTY 120
MYCAALESLINVSDCSAIQRTQRMKALCSQKPAAGQISSERSRDTKIEVIQLVKNLLTY
Sbjct: 61 MYCAALESLINVSDCSAIQRTQRMKALCSQKPAAGQISSERSRDTKIEVIQLVKNLLTY 120

Query: 121 VRGVYRHGNFR 131
VRGVYRHGNFR
Sbjct: 121 VRGVYRHGNFR 131

>gi|14573528|gb|AAK68108.1|AF385625_1 (AF385625) interleukin-13 [Sus scrofa]
gi|14594692|gb|AAK68109.2|AF385626_1 (AF385626) interleukin-13 [Sus scrofa]
Length = 131

Score = 179 bits (454), Expect = 4e-45
Identities = 96/131 (73%), Positives = 108/131 (82%), Gaps = 3/131 (2%)

Query: 1 MALWLTVVIALTCLGGLASPSVTPSPT-LKELIEELVNITQNQAS-LCNGSMVWSVNLT 58
MALWLT+VIALTC GGLASP PV P T LKELIEELVNITQNQ + LCNGSMVWSVNLT
Sbjct: 1 MALWLTLVIALTCFGLASPGVPVPHSTALKELIEELVNITQNQKTPLCNGSMVWSVNLT 60

Query: 59 AGM-YCAALESLINVSDCSAIQRTQRMKALCSQKPAAGQISSERSRDTKIEVIQLVKNL 117
M YCAALESLIN+SDCSAIQ+TQRMK ALCS KP + Q+ + RDTKIEV Q VK+L
Sbjct: 61 TSMQYCAALESLINISDCSAIQKTQRMKSALCSHKPPSEQVPGKHIRDTKIEVAQFVKDL 120

Query: 118 LTYVRGVYRHG 128
L ++R ++RHG
Sbjct: 121 LKHLRMIFRHG 131

>gi|2905620|gb|AAC03535.1| (AF043334) interleukin 13 precursor [Homo sapiens]

Length = 132

Score = 169 bits (428), Expect = 4e-42

Identities = 94/131 (71%), Positives = 105/131 (79%), Gaps = 1/131 (0%)

Query: 1 MALWLTVVIALTCLGGLASPSVTPSPSTLKELIEELVNITQNQ-ASLCNGSMVWSVNLTA 59
MAL LT VIALTCLGG ASP PV PS L+ELIEELVNITQNQ A LCNGSMVWS+NLTA
Sbjct: 1 MALLLTTVIALTCLGGFASPGVPPSTALRELIEELVNITQNQKAPLCNGSMVWSINLTA 60

Query: 60 GMYCAALESLINVSDCSAIQRTQRMKALCSQKPAAGQISSERSRDTKIEVIQLVKNLLT 119
GMYCAALESLINVS CSAI++TQRM C K +AGQ SS RDTKIEV Q VK+LL
Sbjct: 61 GMYCAALESLINVSGCSAIEKTQRMKLGFCPHKVSAGQFSSLHVRDTKIEVAQFVKDLLL 120

Query: 120 YVRGVYRHGNF 130
+++ ++R G F
Sbjct: 121 HLKCLFREGRF 131

>[gi|4504645|ref|NP_002179.1|](#) (NM_002188) interleukin 13 [Homo sapiens]
[gi|15297318|ref|XP_054534.1|](#) (XM_054534) interleukin 13 [Homo sapiens]
[gi|15297320|ref|XP_054533.1|](#) (XM_054533) hypothetical protein XP_054533 [Homo sapie
* [gi|16171723|ref|XP_055221.1|](#) (XM_055221) hypothetical protein XP_055221 [Homo sapie
[gi|462408|sp|P35225|IL13_HUMAN](#) INTERLEUKIN-13 PRECURSOR (IL-13)
[gi|186276|gb|AAA36107.1|](#) (L06801) interleukin 13 [Homo sapiens]
[gi|673420|emb|CAA48824.1|](#) (X69079) alternative; ATG at 15 is an alternative start c
sapiens]
[gi|1045452|gb|AAB01681.1|](#) (U31120) interleukin-13 precursor [Homo sapiens]
[gi|14091716|gb|AAK53823.1|AF377331.1](#) (AF377331) interleukin 13 [Homo sapiens]
Length = 132

Score = 169 bits (427), Expect = 5e-42

Identities = 94/131 (71%), Positives = 105/131 (79%), Gaps = 1/131 (0%)

Query: 1 MALWLTVVIALTCLGGLASPSVTPSPSTLKELIEELVNITQNQ-ASLCNGSMVWSVNLTA 59
MAL LT VIALTCLGG ASP PV PS L+ELIEELVNITQNQ A LCNGSMVWS+NLTA
Sbjct: 1 MALLLTTVIALTCLGGFASPGVPPSTALRELIEELVNITQNQKAPLCNGSMVWSINLTA 60

Query: 60 GMYCAALESLINVSDCSAIQRTQRMKALCSQKPAAGQISSERSRDTKIEVIQLVKNLLT 119
GMYCAALESLINVS CSAI++TQRM C K +AGQ SS RDTKIEV Q VK+LL
Sbjct: 61 GMYCAALESLINVSGCSAIEKTQRMKLGFCPHKVSAGQFSSLHVRDTKIEVAQFVKDLLL 120

Query: 120 YVRGVYRHGNF 130
+++ ++R G F
Sbjct: 121 HLKCLFREGRF 131

>[gi|2144691|pir|A47481](#) interleukin-13 precursor - human
[gi|580330|emb|CAA48823.1|](#) (X69079) alternative; ATG at 15 is an alternative start c
sapiens]
[gi|445575|prf|1909326A](#) interleukin 13 [Homo sapiens]
Length = 146

Score = 167 bits (424), Expect = 1e-41

Identities = 94/131 (71%), Positives = 105/131 (79%), Gaps = 1/131 (0%)

Query: 1 MALWLTVVIALTCLGGLASPSVTPSPSTLKELIEELVNITQNQ-ASLCNGSMVWSVNLTA 59
MAL LT VIALTCLGG ASP PV PS L+ELIEELVNITQNQ A LCNGSMVWS+NLTA
Sbjct: 15 MALLLTTVIALTCLGGFASPGVPPSTALRELIEELVNITQNQKAPLCNGSMVWSINLTA 74

Query: 60 GMYCAALESLINVSDCSAIQRTQRM LKALCSQKPAAGQISSERSRDTKIEVIQLVKNLLT 119
 GMYCAALESLINVS CSAI++TQRM L C K +AGQ SS RDTKIEV Q VK+LL
 Sbjct: 75 GMYCAALESLINVSGCSAIEKTQRM LSGFCPHKVSAGQFSSLHVRDTKIEVAQFVKDLLL 134

Query: 120 YVRGVYRHGNF 130
 +++ ++R G F
 Sbjct: 135 HLKKLFRGRF 145

>[gi|7387804|sp|Q9XSV9|IL13_BOVIN](#) INTERLEUKIN-13 PRECURSOR (IL-13)
[gi|5420145|emb|CAB46636.1|](#) (AJ132441) interleukin-13 [Bos taurus]
 Length = 132

Score = 161 bits (408), Expect = 8e-40
 Identities = 87/131 (66%), Positives = 103/131 (78%), Gaps = 1/131 (0%)

Query: 1 MALWLTVVIALTCLGGLASPSPTLKE LIEELVNITQNQ-ASLCNGSMVWSVNLTA 59
 MAL LT VI L C GGL SPSPV + LKE LIEELVNITQNQ LCNGSMVWS+NLTA
 Sbjct: 1 MALLLTAVIVLICFGLTSPSPVPSATALKE LIEELVNITQNQKVPLCNGSMVWSLNLTS 60

Query: 60 GMYCAALESLINVSDCSAIQRTQRM LKALCSQKPAAGQISSERSRDTKIEVIQLVKNLLT 119
 MYCAAL+SLI++S+CS IQRT++ML ALC KP+A Q+SSE RDTKIEV Q +K+LL
 Sbjct: 61 SMYCAALDSLISISNCSVIQRTKKMLNALCPHKPSAKQVSSEYVRDTKIEVAQFLKDLLR 120

Query: 120 YVRGVYRHGNF 130
 + R V+R+ F
 Sbjct: 121 HSRIVFRNERF 131

>[gi|1127548|gb|AAA83738.1|](#) (U10307) interleukin 13 [Homo sapiens]
 Length = 131

Score = 160 bits (406), Expect = 1e-39
 Identities = 92/131 (70%), Positives = 103/131 (78%), Gaps = 2/131 (1%)

Query: 1 MALWLTVVIALTCLGGLASPSPTLKE LIEELVNITQNQAS-LCNGSMVWSVNLTA 59
 MAL LT VIALTCLGG ASP PV PS L+ELIEELVNITQNQ LCNGSMVWS+NLTA
 Sbjct: 1 MALLLTVVIALTCLGGFASPGFPVPSTALRELIEELVNITQNQKRPLCNGSMVWSINLTA 60

Query: 60 GMYCAALESLINVSDCSAIQRTQRM LKALCSQKPAAGQISSERSRDTKIEVIQLVKNLLT 119
 GMYCAALESLINVS CSAI++TQRM L C K +AG SS RDTKIEV Q VK+LL
 Sbjct: 61 GMYCAALESLINVSGCSAIEKTQRM LSGFCPHKVSAG-FSSLHVRDTKIEVAQFVKDLLL 119

Query: 120 YVRGVYRHGNF 130
 +++ ++R G F
 Sbjct: 120 HLKKLFRGRF 130

>[gi|4558814|gb|AAD22748.1|AF072807_1](#) (AF072807) interleukin-13 precursor [Bos taurus]
 Length = 114

Score = 146 bits (368), Expect = 3e-35
 Identities = 81/113 (71%), Positives = 91/113 (79%), Gaps = 1/113 (0%)

Query: 1 MALWLTVVIALTCLGGLASPSPTLKE LIEELVNITQNQ-ASLCNGSMVWSVNLTA 59
 MAL LT VI L C GGL SPSPV + LKE LIEELVNITQNQ LCNGSMVWS+NLTA

Sbjct: 1 MALLLTAVIVLICFGGLTSPSPVPSATALKELIEELVNITQNQKVPLCNGSMVWSLNLTS 60

Query: 60 GMYCAALESLINVSDCSAIQRTQRMKALCSQKPAAGQISSERSRDTKIEVIQ 112
MYCAAL+SLI++S+CS IQRT+RML ALC KP+A Q+SSE RDTKIEV Q

Sbjct: 61 SMYCAALDSLISISNCSVIQRTKRMLNALCPHKPSAKQVSSEYVRDTKIEVAQ 113

>[gi|6680403|ref|NP_032381.1|](#) (NM_008355) interleukin 13 [Mus musculus]
[gi|129377|sp|P20109|IL13_MOUSE](#) INTERLEUKIN-13 PRECURSOR (IL-13) (T-CELL ACTIVATION
[gi|91336|pir|E30552](#) T-cell activation protein P600 precursor - mouse
[gi|533247|gb|AAA40149.1|](#) (M23504) T cell secreted protein [Mus musculus]
Length = 131

Score = 143 bits (360), Expect = 3e-34

Identities = 79/134 (58%), Positives = 98/134 (72%), Gaps = 7/134 (5%)

Query: 1 MALWLTVVIALTCLGGLASPSVTPSP----TLKELIEELVNITQNQASLCNGSMVWSVN 56
MALW+T V+AL CLGGLA+P PV S TLKELIEEL NITQ+Q LCNGSMVWSV+

Sbjct: 1 MALWVTAVLALACLGGLAAPGPVPRSVSLPLTLKELIEELSNITQDQTPLCNGSMVWSVD 60

Query: 57 LTAGMYCAALESLINVSDCSAIQRTQRMKALCSQKPAAGQISSERSRDTKIEVIQLVKN 116
L AG +C AL+SL N+S+C+AI RTQR+L LC++K A +SS DTKIEV +

Sbjct: 61 LAAGGFCVALDSL TNISNCNAIYRTQRILHGLCNRK-APTTVSS--LPDTKIEVAHFITK 117

Query: 117 LLTYVRGVYRHGNF 130

LL+Y + ++RHG F

Sbjct: 118 LLSYTKQLFRHGPF 131

>[gi|14719448|pdb|1GA3|A](#) Chain A, Nmr Structure Of Interleukin-13
Length = 113

Score = 141 bits (355), Expect = 1e-33

Identities = 77/110 (70%), Positives = 88/110 (80%), Gaps = 1/110 (0%)

Query: 22 PVTPSPTLKELIEELVNITQNQ-ASLCNGSMVWSVNLTAGMYCAALESLINVSDCSAIQR 80
PV PS L+ELIEELVNITQNQ A LCNGSMVWS+NLTAGMYCAALESLINVS CSAI++

Sbjct: 3 PVPPSTALRELIEELVNITQNQKAPLCNGSMVWSINLTAGMYCAALESLINVSGCSAIEK 62

Query: 81 TQRMKALCSQKPAAGQISSERSRDTKIEVIQLVKNLLTYVRGVYRHGNF 130
TQRM L C K +AGQ SS RDTKIEV Q VK+LL +++ ++R G F

Sbjct: 63 TQRM LSGFCPHKVSAGQFSSLHVRDTKIEVAQFVKDLLLHLKKLFREGRF 112

>[gi|16758680|ref|NP_446280.1|](#) (NM_053828) interleukin 13 [Rattus norvegicus]
[gi|1170528|sp|P42203|IL13_RAT](#) INTERLEUKIN-13 PRECURSOR (IL-13) (T-CELL ACTIVATION P
[gi|2118664|pir|I52290](#) interleukin-13 - rat
[gi|438876|gb|AAA16478.1|](#) (L26913) interleukin-13 [Rattus norvegicus]
Length = 131

Score = 139 bits (350), Expect = 4e-33

Identities = 79/134 (58%), Positives = 99/134 (72%), Gaps = 8/134 (5%)

Query: 1 MALWLTVVIALTCLGGLASPSV----TPSPTLKELIEELVNITQNQ-ASLCNGSMVWSV 55
MALW+T V+AL CLGGLA+P PV +P L+ELIEEL NITQ+Q SLCN SMVWSV

Sbjct: 1 MALWVTAVLALACLGGLATPGPVRRSTSPVALRELIEELSNITQDQKTSLCNSSMVWSV 60

Query: 56 NLTAGMYCAALES LINVSDCSAIQRTQRM LKALCSQKPAAGQISSERSRDTKIEVIQLVK 115
 +LTAG +CAALES L N+S C+AI RTQR+L LC+QK A ++S DTKIEV Q +
 Sbjct: 61 DLTAGGFCAALES LTNISSCNAIHRTQRILNGLCNQK--ASDVASS-PPDTKIEVAQFIS 117

Query: 116 NLLTYVRGVYRHGN 129
 LL Y + ++R+G+
 Sbjct: 118 KLLNYSKQLFRYGH 131

>gi|258577|gb|AAB23881.1| P600 homolog [human, Peptide, 49 aa]
 Length = 49

Score = 61.2 bits (147), Expect = 1e-09
 Identities = 35/49 (71%), Positives = 36/49 (73%), Gaps = 1/49 (2%)

Query: 1 MALWLTVVIALTCLGGLASPSVTPSPSTLKE LIEELVNITQ NQ-ASLCN 48
 MAL LT VIAL CLGG SP PV PS L+ELIEEL NITQ Q A LCN
 Sbjct: 1 MALLLTTVIALACLGFDSPGPVPPSTALRELIEELS NITQTQKAPLCN 49

>gi|451840|gb|AAA61629.1| (U05203) putative preprosperminogen [Oryctolagus cuniculus]
 Length = 275

Score = 31.2 bits (69), Expect = 1.8
 Identities = 21/71 (29%), Positives = 33/71 (45%), Gaps = 6/71 (8%)

Query: 16 GLASPSVTPSPSTLKE LIEELVNITQ NQASLCNGSMVSVNLTAGMYCAALES LINVSDC 75
 G + PSPTL E +L+N+ LCN + ++ +TA CA S + C
 Sbjct: 181 GYVKENAPRPSPTLMEARVDLINL-----ELCNSTQWYNGRITASNL CAGYPSG-KIDTC 234

Query: 76 SAIQRTQRM LK 86
 +Q+ +LK
 Sbjct: 235 QRLQQLVEVLK 245

>gi|16760873|ref|NP_456490.1| (NC_003198) flagellar transcriptional activator [Salmo
 enterica subsp. enterica serovar Typhi]
gi|16503170|emb|CAD05675.1| (AL627272) flagellar transcriptional activator [Salmo
 subsp. enterica serovar Typhi]
 Length = 194

Score = 31.2 bits (69), Expect = 1.8
 Identities = 16/56 (28%), Positives = 26/56 (45%), Gaps = 3/56 (5%)

Query: 51 MVWSVNLTAGMYCAALES LINVSDCS---AIQRTQRM LKALCSQKPAAGQISSERS 103
 M W N+ A M+C A + L+ CS A+ + R+ C Q P ++ R+
 Sbjct: 67 MTWEQNIHASMFCNAWQFLKLTGLCSGVDAVIKAYRLYLEQCPQPPEGSLALTRA 122

>gi|7387658|sp|O52222|FLHC_SALTY FLAGELLAR TRANSCRIPTIONAL ACTIVATOR FLHC
gi|2772918|gb|AAB96640.1| (AF029300) FlhC [Salmonella typhimurium]
gi|6045176|dbj|BAA85315.1| (D43640) FlhC protein [Salmonella typhimurium]
 Length = 192

Score = 30.4 bits (67), Expect = 2.8
 Identities = 16/56 (28%), Positives = 26/56 (45%), Gaps = 3/56 (5%)

Sbjct: 44 ALECLGGVSGGGITDYNPALRSRLTIMKDDSKNQVSLSLSSV--TLEDATATYYCA 96

>gi|15641617|ref|NP_231249.1| (NC_002505) conserved hypothetical protein [Vibrio cholerae (group O1 strain N16961)] - Vibrio
 gi|11354623|pir|C82178 conserved hypothetical protein VC1609 [imported] - Vibrio
 gi|9656121|gb|AAF94763.1| (AE004238) conserved hypothetical protein [Vibrio cholera]
 Length = 408

Score = 28.9 bits (63), Expect = 8.0

Identities = 18/48 (37%), Positives = 27/48 (55%), Gaps = 4/48 (8%)

Query: 2 ALWLTVVIALTCLGGLASPSVTPSPSTLKELEE-----LVNITQNQAS 45

AL+ V+ LT GG+ S + P P K++ E +VN+ Q+QAS

Sbjct: 39 ALFTNPVVVLTVFGGVVFYSFLYPLPYAKQIPREQTVSVVNLDQSQAS 86

Database: nr

Posted date: Nov 16, 2001 11:40 PM

Number of letters in database: 254,026,857

Number of sequences in database: 799,241

Lambda	K	H
0.319	0.131	0.381

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 60,265,884

Number of Sequences: 799241

Number of extensions: 1930804

Number of successful extensions: 5801

Number of sequences better than 10.0: 32

Number of HSP's better than 10.0 without gapping: 17

Number of HSP's successfully gapped in prelim test: 15

Number of HSP's that attempted gapping in prelim test: 5767

Number of HSP's gapped (non-prelim): 32

length of query: 131

length of database: 254,026,857

effective HSP length: 107

effective length of query: 24

effective length of database: 168,508,070

effective search space: 4044193680

effective search space used: 4044193680

T: 11

A: 40

X1: 16 (7.4 bits)

X2: 38 (14.6 bits)

X3: 64 (24.7 bits)

S1: 41 (21.8 bits)

S2: 63 (28.9 bits)



PubMed

Nucleotide

Protein

Genome

Structure

PopSet

Taxonomy

OMIM

Bio

Search for

Go

Clear

Limits

Preview/Index

History

Clipboard

Details

Display

GenPept

Save

Text

Add to Clipboard

☐ 1: P35225. INTERLEUKIN-13 PR...
[gi:462408]

BLink, Related Sequences, OMIM, PubMed, Taxonomy,
LinkOut

LOCUS IL13_HUMAN 132 aa PRI 20-AUG-2001

DEFINITION INTERLEUKIN-13 PRECURSOR (IL-13).

* ACCESSION P35225

PID g462408

VERSION P35225 GI:462408

DBSOURCE swissprot: locus IL13_HUMAN, accession P35225;
class: standard.
extra accessions:043644,created: Feb 1, 1994.
sequence updated: Feb 1, 1994.
annotation updated: Aug 20, 2001.
xrefs: gi: gi: [186275](#), gi: gi: [186276](#), gi: gi: [297787](#), gi: gi:
[673420](#), gi: gi: [580330](#), gi: gi: [1045451](#), gi: gi: [1045452](#), gi: gi:
[505626](#), gi: gi: [1127548](#), gi: gi: [2905619](#), gi: gi: [2905620](#), gi: gi:
[2144691](#), gi: gi: [1421355](#), gi: gi: [1421358](#)
xrefs (non-sequence databases): MIM [147683](#), InterPro IPR003634,
InterPro IPR001325, ProDom PD015987, PROSITE PS00838

KEYWORDS Cytokine; Glycoprotein; Signal; 3D-structure; Polymorphism.

SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (residues 1 to 132)

AUTHORS Minty,A.J., Chalon,P., Derocq,J.M., Dumont,X., Guillemot,J.C.,
Kaghad,M., Labit,C., Leplatois,P., Liauzun,P., Miloux,B., Minty,C.,
Casellas,P., Loison,G., Lupker,J., Shire,D., Ferrara,P. and
Caput,D.

TITLE Interleukin-13 is a new human lymphokine regulating inflammatory
and immune responses

JOURNAL Nature 362 (6417), 248-250 (1993)

MEDLINE [93211479](#)

REMARK SEQUENCE FROM N.A.

REFERENCE 2 (residues 1 to 132)

AUTHORS McKenzie,A.N., Culpepper,J.A., Waal Malefyt,R., Briere,F.,
Punnonen,J., Aversa,G., Sato,A., Dang,W., Cocks,B.G., Menon,S., de
Vries,J.E., Banchereau,J. and Zurawski,G.R.

TITLE Interleukin 13, a T-cell-derived cytokine that regulates human
monocyte and B-cell function

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 90 (8), 3735-3739 (1993)

MEDLINE [93234572](#)

REMARK SEQUENCE FROM N.A.

REFERENCE 3 (residues 1 to 132)

AUTHORS Dolganov,G., Lewis,D.B., Lovett,M., Burr,J., Bort,S., Short,D.,
McGurn,M. and Gibson,C.

TITLE Direct Submission

JOURNAL Submitted (??-JUL-1995)

REMARK SEQUENCE FROM N.A.


```
Region      45
             /region_name="Conflict"
             /note="A -> R (IN REF. 4)."
Bond        bond(48,76)
             /bond_type="disulfide"
Site        49
             /site_type="glycosylation"
             /note="N-LINKED (GLCNAC...) (POTENTIAL)."
Site        57
             /site_type="glycosylation"
             /note="N-LINKED (GLCNAC...) (POTENTIAL)."
Bond        bond(64,90)
             /bond_type="disulfide"
Site        72
             /site_type="glycosylation"
             /note="N-LINKED (GLCNAC...) (POTENTIAL)."
Region      87
             /region_name="Conflict"
             /note="S -> G (IN REF. 5)."
Region      98
             /region_name="Conflict"
             /note="MISSING (IN REF. 4)."
Region     130
             /region_name="Variant"
             /note="R -> Q. /FTId=VAR_010037."
ORIGIN
      1 malllttvia ltcclggfasp gvpvpstaln elieelnit qnqkaplcng smvwsinlta
     61 gmycaalesl invsgcsaie ktqrmlsgfc phkvsagqfs slhvrtdkie vaqfvkdlll
    121 hlkklfregr fn
//
```

Revised: October 24, 2001.

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